

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/559,806  
Source: IFWP  
Date Processed by STIC: 12/16/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/559,806

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4      Non-ASCII      The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                                 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                 This sequence is intentionally skipped  
  
                                 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                                 <210> sequence id number  
                                 <400> sequence id number  
                                 000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                                 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence.
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                                 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. **This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).** Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n/Xaa      "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

## RAW SEQUENCE LISTING

DATE: 12/16/2005

PATENT APPLICATION: US/10/559,806

TIME: 15:04:30

Input Set : A:\Q91925 sequence listing.txt

Output Set: N:\CRF4\12162005\J559806.raw

3 <110> APPLICANT: TOOLGEN, INC, et al.  
 5 <120> TITLE OF INVENTION: Transducible DNA-Binding Proteins  
 7 <130> FILE REFERENCE: Q91925  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/559,806  
 C--> 9 <141> CURRENT FILING DATE: 2005-12-08  
 9 <150> PRIOR APPLICATION NUMBER: US 60/477,459  
 10 <151> PRIOR FILING DATE: 2003-06-10  
 12 <160> NUMBER OF SEQ ID NOS: 72  
 14 <170> SOFTWARE: PatentIn version 3.2

## ERRORED SEQUENCES

1131 <210> SEQ ID NO: 72  
 1132 <211> LENGTH: 11  
 1133 <212> TYPE: PRT  
 1134 <213> ORGANISM: Synthetic  
 1136 <400> SEQUENCE: 72  
 1138 Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala  
 1139 1 5 10  
 E--> 1142 30  
 E--> 1144 1 delete

*invalid <213> response*  
*Does Not Comply*  
*Corrected Diskette Needed*  
*(see item 10 on Error Summary Sheet)*

*→ This error appears in other sequences, too.*

*see p. 2*

<210> 5  
<211> 26  
<212> PRT  
<213> Artificial Sequence

<220>

<223> coordinating residue

insufficient explanation - give source  
of genetic  
material

(see item 11 on  
Error Summary  
Sheet)

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/559,806

DATE: 12/16/2005

TIME: 15:04:31

Input Set : A:\Q91925 sequence listing.txt

Output Set: N:\CRF4\12162005\J559806.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:16  
L:117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0  
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:16  
L:415 M:283 W: Missing Blank Line separator, <400> field identifier  
L:553 M:283 W: Missing Blank Line separator, <400> field identifier  
L:691 M:283 W: Missing Blank Line separator, <400> field identifier  
L:829 M:283 W: Missing Blank Line separator, <400> field identifier  
L:967 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1142 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:72  
L:1144 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:72